RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10 648 825 A

Source: IFWL6

Date Processed by STIC: 5/24/5

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IFW16

RAW SEQUENCE LISTING   DATE: 05/24/2005
PATENT APPLICATION: US/10/648,825A   TIME: 08:56:09

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF4\05242005\J648825A.raw

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 3 <110> APPLICANT: Ni, Jian
 4       Gentz, Reiner L
 5       Yu, Guo-Liang
 6       Su, Jeffrey
 7       Rosen, Craig A
 9 <120> TITLE OF INVENTION: Death Domain Containing Receptor 5
11 <130> FILE REFERENCE: 1488.131000C
13 <140> CURRENT APPLICATION NUMBER: 10/648,825A
14 <141> CURRENT FILING DATE: 2003-08-27
16 <150> PRIOR APPLICATION NUMBER: 60/040,846
17 <151> PRIOR FILING DATE: 1997-03-17
19 <150> PRIOR APPLICATION NUMBER: 60/054,021
20 <151> PRIOR FILING DATE: 1997-07-29
22 <150> PRIOR APPLICATION NUMBER: 09/042,538
23 <151> PRIOR FILING DATE: 1998-03-17
25 <150> PRIOR APPLICATION NUMBER: 60/132,498
26 <151> PRIOR FILING DATE: 1998-05-04
28 <150> PRIOR APPLICATION NUMBER: 60/133,238
29 <151> PRIOR FILING DATE: 1998-05-07
31 <150> PRIOR APPLICATION NUMBER: 60/148,939
32 <151> PRIOR FILING DATE: 1998-08-13
34 <150> PRIOR APPLICATION NUMBER: 09/565,009
35 <151> PRIOR FILING DATE: 2000-05-04
37 <150> PRIOR APPLICATION NUMBER: 60/406,307
38 <151> PRIOR FILING DATE: 2002-08-28
40 <150> PRIOR APPLICATION NUMBER: 60/413,747
41 <151> PRIOR FILING DATE: 2002-09-27
43 <160> NUMBER OF SEQ ID NOS: 14
45 <170> SOFTWARE: PatentIn version 3.1
47 <210> SEQ ID NO: 1
48 <211> LENGTH: 1600
49 <212> TYPE: DNA
50 <213> ORGANISM: Homo sapiens
53 <220> FEATURE:
54 <221> NAME/KEY: CDS
55 <222> LOCATION: (130)..(1362)
57 <220> FEATURE:
58 <221> NAME/KEY: sig_peptide
59 <222> LOCATION: (130)..(282)
61 <220> FEATURE:
62 <221> NAME/KEY: mat_peptide
63 <222> LOCATION: (283)..(1362)
65 <400> SEQUENCE: 1
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66 cacgcgtccg cgggcgcggc cggagaaccc cgcaatcttt gcgcccacaa aatacaccga     60
68 cgatgcccga tctactttaa gggctgaaac ccacgggcct gagagactat aagagcgttc    120
70 cctaccgcc atg gaa caa cgg gga cag aac gcc ccg gcc gct tcg ggg gcc    171
71          Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala
72              -50                 -45                 -40
74 cgg aaa agg cac ggc cca gga ccc agg gag gcg cgg gga gcc agg cct    219
75 Arg Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro
76         -35                 -30                 -25
78 ggg ccc cgg gtc ccc aag acc ctt gtg ctc gtt gtc gcc gcg gtc ctg    267
79 Gly Pro Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu
80     -20                 -15                 -10
82 ctg ttg gtc tca gct gag tct gct ctg atc acc caa caa gac cta gct    315
83 Leu Leu Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala
84 -5             -1  1                5                   10
86 ccc cag cag aga gcg gcc cca caa caa aag agg tcc agc ccc tca gag    363
87 Pro Gln Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu
88         15                  20                  25
90 gga ttg tgt cca cct gga cac cat atc tca gaa gac ggt aga gat tgc    411
91 Gly Leu Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys
92         30                  35                  40
94 atc tcc tgc aaa tat gga cag gac tat agc act cac tgg aat gac ctc    459
95 Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu
96     45                  50                  55
98 ctt ttc tgc ttg cgc tgc acc agg tgt gat tca ggt gaa gtg gag cta    507
99 Leu Phe Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu
100 60                 65                  70                  75
102 agt ccc tgc acc acg acc aga aac aca gtg tgt cag tgc gaa gaa ggc   555
103 Ser Pro Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly
104                80                  85                  90
106 acc ttc cgg gaa gaa gat tct cct gag atg tgc cgg aag tgc cgc aca   603
107 Thr Phe Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr
108             95                  100                 105
110 ggg tgt ccc aga ggg atg gtc aag gtc ggt gat tgt aca ccc tgg agt   651
111 Gly Cys Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser
112         110                 115                 120
114 gac atc gaa tgt gtc cac aaa gaa tca ggc atc atc ata gga gtc aca   699
115 Asp Ile Glu Cys Val His Lys Glu Ser Gly Ile Ile Ile Gly Val Thr
116     125                 130                 135
118 gtt gca gcc gta gtc ttg att gtg gct gtg ttt gtt tgc aag tct tta   747
119 Val Ala Ala Val Val Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu
120 140                 145                 150                 155
122 ctg tgg aag aaa gtc ctt cct tac ctg aaa ggc atc tgc tca ggt ggt   795
123 Leu Trp Lys Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly
124                 160                 165                 170
126 ggt ggg gac cct gag cgt gtg gac aga agc tca caa cga cct ggg gct   843
127 Gly Gly Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala
128             175                 180                 185
130 gag gac aat gtc ctc aat gag atc gtg agt atc ttg cag ccc acc cag   891
131 Glu Asp Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln
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132        190                    195                    200
134 gtc cct gag cag gaa atg gaa gtc cag gag cca gca gag cca aca ggt    939
135 Val Pro Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly
136     205                    210                    215
138 gtc aac atg ttg tcc ccc ggg gag tca gag cat ctg ctg gaa ccg gca    987
139 Val Asn Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala
140 220                    225                    230                    235
142 gaa gct gaa agg tct cag agg agg agg ctg ctg gtt cca gca aat gaa   1035
143 Glu Ala Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn Glu
144                    240                    245                    250
146 ggt gat ccc act gag act ctg aga cag tgc ttc gat gac ttt gca gac   1083
147 Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp
148                    255                    260                    265
150 ttg gtg ccc ttt gac tcc tgg gag ccg ctc atg agg aag ttg ggc ctc   1131
151 Leu Val Pro Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu
152     270                    275                    280
154 atg gac aat gag ata aag gtg gct aaa gct gag gca gcg ggc cac agg   1179
155 Met Asp Asn Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg
156     285                    290                    295
158 gac acc ttg tac acg atg ctg ata aag tgg gtc aac aaa acc ggg cga   1227
159 Asp Thr Leu Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg
160 300                    305                    310                    315
162 gat gcc tct gtc cac acc ctg ctg gat gcc ttg gag acg ctg gga gag   1275
163 Asp Ala Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu
164                    320                    325                    330
166 aga ctt gcc aag cag aag att gag gac cac ttg ttg agc tct gga aag   1323
167 Arg Leu Ala Lys Gln Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys
168                    335                    340                    345
170 ttc atg tat cta gaa ggt aat gca gac tct gcc atg tcc taagtgtgat   1372
171 Phe Met Tyr Leu Glu Gly Asn Ala Asp Ser Ala Met Ser
172            350                    355                    360
174 tctcttcagg aagtgagacc ttccctggtt tacctttttt ctggaaaaag cccaactgga   1432
176 ctccagtcag taggaaagtg ccacaattgt cacatgaccg gtactggaag aaactctccc   1492
178 atccaacatc acccagtgga tggaacatcc tgtaactttt cactgcactt ggcattattt   1552
180 ttataagctg aatgtgataa taaggacact atggaaaaaa aaaaaaaa                 1600
183 <210> SEQ ID NO: 2
184 <211> LENGTH: 411
185 <212> TYPE: PRT
186 <213> ORGANISM: Homo sapiens
188 <400> SEQUENCE: 2
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194 Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Pro
195 -35                    -30                    -25                    -20
198 Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu
199                    -15                    -10                    -5
202 Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln
203            -1  1                    5                    10
206 Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
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207      15                  20                  25
210 Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser
211 30                  35                  40                  45
214 Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe
215                 50                  55                  60
218 Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro
219                 65                  70                  75
222 Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe
223         80                  85                  90
226 Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys
227     95                  100                 105
230 Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile
231 110    .             115                 120                 125
234 Glu Cys Val His Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala
235                 130                 135                 140
238 Ala Val Val Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp
239                 145                 150                 155
242 Lys Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly
243         160                 165                 170
246 Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp
247     175                 180                  .    185
250 Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro
251 190                 195                 200                 205
254 Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn
255                 210                 215                 220
258 Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala
259             225                 230                 235
262 Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn Glu Gly Asp
263         240                 245                 250
266 Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val
267     255                 260                 265
270 Pro Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp
271 270                 275                 280                 285
274 Asn Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr
275                 290                 295                 300
278·Leu Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala
279             305                 310                 315
282 Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu
283         320                 325                 330·
286 Ala Lys Gln Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met
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290 Tyr Leu Glu Gly Asn Ala Asp Ser Ala Met Ser
291 350             355                 360
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298 <211> LENGTH: 455
299 <212> TYPE: PRT
300 <213> ORGANISM: human
302 <400> SEQUENCE: 3
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305 1                   5                   10                  15
307 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
308             20                  25                  30
310 His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
311         35                  40                  45
313 Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
314     50                  55                  60
316 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
317 65                  70                  75                  80
319 Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
320             85                  90                  95
322 Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
323             100                 105                 110
325 Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
326             115                 120                 125
328 Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
329     130                 135                 140
331 Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
332 145                 150                 155                 160
334 Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
335             165                 170                 175
337 Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
338             180                 185                 190
340 Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
341         195                 200                 205
344 Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
345     210                 215                 220
347 Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
348 225                 230                 235                 240
350 Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
351             245                 250                 255
353 Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
354             260                 265                 270
356 Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
357         275                 280                 285
359 Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
360     290                 295                 300
362 Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
363 305                 310                 315                 320
365 Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
366             325                 330                 335
368 Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
369             340                 345                 350
371 Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
372         355                 360                 365
374 Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
375     370                 375                 380
377 Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
378 385                 390                 395                 400
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 05/24/2005
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<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:6; N Pos. 152,199,272,285,310,322,329,331,344,353,363,368,370,374,376
Seq#:6; N Pos. 388,393,403,407,409,410,414,416,421,424,426,451,452,462,463
Seq#:6; N Pos. 466,468,469,471,486,489,495,497,502,503,504
Seq#:14; N Pos. 37,79,81,124,233

VERIFICATION SUMMARY   DATE: 05/24/2005
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Input Set : **A:\Sequence Listing.txt**
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L:740 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:120
M:341 Repeated in SeqNo=6
L:879 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
M:341 Repeated in SeqNo=14